

Supplementary Online Content

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eAppendix. Supplementary Methods.

This supplementary material has been provided by the authors to give readers additional information about their work.

SUPPLEMENTARY METHODS

VBM

Data Processing. Normalization parameters comprised a 12-parameter affine transformation and nonlinear normalization using $7 \times 8 \times 7$ basis functions. Smoothing was done with an isotropic Gaussian kernel with FWHM of 8 mm. Gray and white matter partitions were spatially normalized (12-parameter affine transformation and $7 \times 8 \times 7$ basis functions). The deformation parameters obtained from the normalization process of gray and white matter partitions were applied to the original raw images in native space to create optimally normalized whole-brain images, which were recursively segmented. Jacobian modulated (reflecting gray and white matter volume) images were smoothed with a kernel with a FWHM of 12 mm. Jacobian determinants of the spatial transformation matrix (an index of the amount of volumetric compression that each voxel is subjected to when stretching, shearing and compressing the images into stereotaxic space^{1,2}) and total gray and white matter volumes were compared between groups to avoid confounding effects due to difference in shapes and gray and white matter volumes. There were no significant differences in the Jacobian determinants, total gray or white matter volumes.

DTI

Image Processing. All individual images were then visually inspected to discard slices with motion artifacts, after which the remaining images were added for each slice. The pixel intensities of the multiple diffusion-weighted images were then fitted to obtain the twelve elements of the symmetric diffusion tensor. The diffusion tensors at each pixel were diagonalized to obtain pixel eigenvalues and eigenvectors. Fractional anisotropy (FA) maps, average non-diffusion weighted images ($b = 0$ s/mm²), average diffusion coefficient images (ADC, $b = 815$ s/mm²) and primary eigenvectors (eigenvector (v_1) associated with the largest eigenvalue (λ_1) was assumed to represent the local fiber direction of the diffusion tensor were obtained for further analyses.

Region of Interest (ROI) Selection. Specifically, binary masks of clusters that showed significant difference in connectivity between the two groups were constructed and then registered to each individual subjects' b_0 image. For each participant, two sets of ROIs were used to perform tractography analysis. The first set of ROIs was derived directly from the observed clusters of significant between-group (HIGH vs. LOW) functional connectivity. The second set of ROIs was also derived from the observed clusters of significant between-group functional connectivity but were dilated 3 mm in order to confirm that each ROI encompassed surrounding white matter³. Fibers were selected that projected through both the dACC and left DLPFC ROIs (un-dilated and dilated separately). For each set of analyses, both ROIs were imported into DTIstudio and fibers projecting through both ROIs were isolated by using the "and" function. Fibers were then visually inspected for anatomical coherence with functional results.

Analyses were repeated using only one ROI (either left DLPFC or dACC) at a time.

Fiber-Tracking. Briefly, tracing was initiated from a seed pixel from which a line was propagated in both retrograde and orthograde directions according to v_1 at each pixel. The tracking was terminated when it reached a voxel with an FA value lower than 0.10^4 , or when the turning angle was greater than 60°^5 . A direct comparison of the fidelity of diffusion-weighted data collected using optimized 6, 10, 15 and 30 direction schemes indicates that each have comparable precision and that they each have sufficient power in order to discriminate normal from abnormal white-matter integrity⁶. In order to reconstruct branching patterns, the tracking was performed from every pixel inside the brain, but only fibers that penetrated ROIs were retained⁷.

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